

N. Doss

1646

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/051,843

DATE: 01/14/1999
TIME: 15:51:49

Input Set: I051843.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Willson, Tracy
2 Nicola, Nicos A.
3 Hilton, Douglas J.
4 Metcalf, Donald
5 Zhang, Jian G.
6 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
7 ENCODING SAME
8 <130> FILE REFERENCE: Davies cc
9 <140> CURRENT APPLICATION NUMBER: US/09/051,843
10 <141> CURRENT FILING DATE: 1998-06-29
11 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 1383
15 <212> TYPE: DNA
16 <213> ORGANISM: nuc. & predicted a.a. seq. of mNR4
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19 <222> LOCATION: (61)..(1338)
20 <220> FEATURE:
21 <221> NAME/KEY: unsure
22 <222> LOCATION: (121)
23 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
24 region
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43 <223> OTHER INFORMATION: n=authors are unsure of exact sequence in this
44 region

ENTERED

new format

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 52 atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108
 53 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Trp
 54 1 5 10 15
 W--> 55 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
 56 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
 57 20 25 30
 58 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
 59 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
 60 35 40 45
 61 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
 62 Trp Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
 63 50 55 60
 64 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
 65 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 66 65 70 75 80
 67 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
 68 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
 69 85 90 95
 70 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
 71 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
 72 100 105 110
 73 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
 74 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 75 115 120 125
 76 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
 77 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 78 130 135 140
 79 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
 80 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
 81 145 150 155 160
 82 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
 83 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
 84 165 170 175
 85 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
 86 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
 87 180 185 190
 88 cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat 684
 89 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
 90 195 200 205
 91 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat 732
 92 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
 93 210 215 220
 94 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt 780

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95 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
 96 225 230 235 240
 97 gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc 828
 98 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
 99 245 250 255
 100 tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat 876
 101 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
 102 260 265 270
 103 att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga 924
 104 Ile Leu Glu Val Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
 105 275 280 285
 106 aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac 972
 107 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
 108 290 295 300
 109 gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt 1020
 110 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
 111 305 310 315 320
 112 gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt 1068
 113 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
 114 325 330 335
 115 aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca 1116
 116 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Met Leu Leu Thr Ile Pro
 117 340 345 350
 118 gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg 1164
 119 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
 120 355 360 365
 121 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt 1212
 122 Leu Lys Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 123 370 375 380
 124 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag 1260
 125 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 126 385 390 395 400
 127 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg 1308
 128 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
 129 405 410 415
 130 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc 1358
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 150 20 25 30
 151 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
 152 35 40 45
 153 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
 154 50 55 60
 155 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 156 65 70 75 80
 157 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
 158 85 90 95
 159 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
 160 100 105 110
 161 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 162 115 120 125
 163 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 164 130 135 140
 165 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
 166 145 150 155 160
 167 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
 168 165 170 175
 169 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
 170 180 185 190
 171 W-->OK Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
 172 195 200 205
 173 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
 174 210 215 220
 175 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
 176 225 230 235 240
 177 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
 178 245 250 255
 179 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
 180 260 265 270
 181 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
 182 275 280 285
 183 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
 184 290 295 300
 185 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
 186 305 310 315 320
 187 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
 188 325 330 335
 189 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Met Leu Leu Thr Ile Pro
 190 340 345 350
 191 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
 192 355 360 365
 193 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 194 370 375 380

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Input Set: I051843.RAW

195 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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 197 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
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 211 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Cys
 212 1 5 10 15
 213 gcc ggc ggc ggg ggc ggg ggc ggc gcg cct acg gaa act cag cca 156
 214 Ala Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
 215 20 25 30
 216 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
 217 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
 218 35 40 45
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 220 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
 221 50 55 60
 222 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
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 224 65 70 75 80
 225 act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
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 227 85 90 95
 228 gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
 229 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
 230 100 105 110
 231 gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
 232 Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 233 115 120 125
 234 act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct 492
 235 Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 236 130 135 140
 237 tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac 540
 238 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
 239 145 150 155 160
 240 tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt 588
 241 Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
 242 165 170 175
 243 aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag 636
 244 Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys

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VERIFICATION SUMMARY
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DATE: 01/14/1999
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Input Set: I051843.RAW

Line ? Error/Warning

Original Text

55 W "N" or "Xaa" used: Feature required
88 W "N" or "Xaa" used: Feature required
149 W "N" or "Xaa" used: Feature required
171 W "N" or "Xaa" used: Feature required

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cct nnn agt ttt gaa cat cag aac gtt caa a
Thr Ala Thr Val Xaa Gly Gln Val Ala Ala A
Pro Xaa Ser Phe Glu His Gln Asn Val Gln I